Specialty Wood Products Research Partnership

MARLBOROUGH RESEARCH CENTRE
Te Rito Hiranga o Wairau

Technical Report

Assessment of NZDFI *Eucalyptus quadrangulata* Breeding Populations

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FOREST GROWERS RESEARCH

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EXECUTIVE SUMMARY

The objective of the NZDFI breeding programme is to define and then exploit the variation in selected traits by identifying and advancing superior families in the breeding populations. *E. quadrangulata* is one of the top three species of interest to the NZ Dryland Forests Initiative. The age 3.5 year assessment of the 2016 breeding trial at Paparoa and assessment of the 2011 breeding trial at Cuddons is reported and concludes that a genetic improvement programme for this species can progress the key traits. Selection between and within the families that are planted in NZDFI *E. quadrangulata* progeny trials will provide improved germplasm for future forest plantings.

INTRODUCTION

In 2011, the first open-pollinated breeding population of *E. quadrangulata* was established in a series of progeny trials to evaluate the differences between individual families. NZDFI's aim is for each breeding population to test a minimum of 100 families per species, however poor flowering in Australia restricted the number of seedlots available at this time. NZDFI purchased open- pollinated families from CSIRO's tree seed centre and 24 families were successfully raised at Morgans Rd Nursery as containerised seedlings. In 2011 progeny tests were established in a single-tree-plot incomplete block design at 4 sites located in Marlborough (hereby known as Cuddons), Wairarapa, Hawkes Bay and north Canterbury.

This breeding population of *E. quadrangulata* was extended in 2015 when Proseed obtained a further 88 families from ATSC and Forestry Corporation. The seed was supplied to Morgans Road Nursery and 83 families produced seedlings for field testing in 2016. Trials are located at the Bradshaw property, Lamberts Valley, Marlborough and the NZ Redwood Company, Paparoa, near Taumaranui. The University of Canterbury deployed 64 seedlings per family for the UC SFF growth strain testing programme based at Murrays Nursery, Woodville (Altaner, 2019).

These collections were from 6 general locations in NSW, Figure 1.

METHODS

Material

Cuddons 2011

Single-tree plots were established of 70 individuals per family, each block has 24 trees and the spacing of the trees was 2.4 m × 1.8 m, 2,312 sph.
The trial was assessed for height at age 1.6 years in April 2013 and again at age 2.3 years in December 2013 for form and DBH. The trial was re-measured for DBH, height and form at the age of 8.9 years in August 2020. The trial has been thinned to approximately 1000 sph.

Paparoa 2016

40 to 50 seedlings per family were planted using a single-tree-plot incomplete block design. Each block is planted with 36 trees at a stocking of 2,312 sph. There are 86 blocks and these are arranged in three general clusters across the site. There is no significant difference in aspect, altitude or soil type between the areas.

Figure 1: Location of family seedlot collections. Mt Skanzi, Giro SF, Sheas Nob SF, Dalmorton, Chealundi SF and Clouds Creek.

Assessments

The DBH was measured and stem form assessed using the NZDFI assessment scale at the Cuddon and Paparoa trials in July/August 2020. A permanent sample plot (PSP) was established in a group of 6 trial blocks at the Paparoa site and will have repeat measurements to monitor growth.

Figure 2: General view of 2016 Paparoa E. quadrangulata trial(above) and 2011 Cuddons E. quadrangulata trial.

Data analysis

The model equation for each trait used an 'individual-tree' mixed model, which included intercept (μ) and provenance (P) as fixed effects, and random effects for replicate (R), incomplete block within replicate (R/B) and additive genetic effect (A). All random effects have zero mean and variances σ_R^2, σ_B^2, σ_A^2 and σ_e^2, while we also assumed that they are independent of each other; that is, their covariance is 0. The residuals (e) were assumed to follow a normal distribution with common variance and independence from each other.

trait = μ + P + R + R/B + A + e

Therefore, the expected value for the response is μ + P. This model predicts additive genetic values for both parents and individual trees, allowing for within-family selection.

Data preparation and analysis used the R statistical computing language (R Core Team 2020) with the asreml-R package for genetic analyses (Butler 2020). All code is available from the second author in the report.

RESULTS

The growth and form data for the Paparoa trial shows considerable differences between the families planted in the trial (Figure 3). The was no relationship between the best families and the location from which they originated in Australia. Therefore, no provenance selection can be applied to future native stand collections.

The age 3.5 year heights were compared across the 3 clusters of blocks planted in the Paparoa trial and no significant variation was calculated. At the time of the 2019 height measurement the crowns had been defoliated at variable severity by Paropsis browsing. The crown health across the trial at the time of the 2020 assessment was good and there has been good growth between measurements.

Tree diameter across all families ranged from 30 to 154mm, the average was 75.6mm. Many stems had multi leaders and heavy branching. This may have been accentuated by insect damage, however as a genetic parameter a high weighting on this selection trait is required to improve the form of successive generations of *E. quadrangulata*.

Tree height measured at the Woodville trial prior to felling and height measurement at age 3.5 years at Paparoa had a correlation of 0.7.

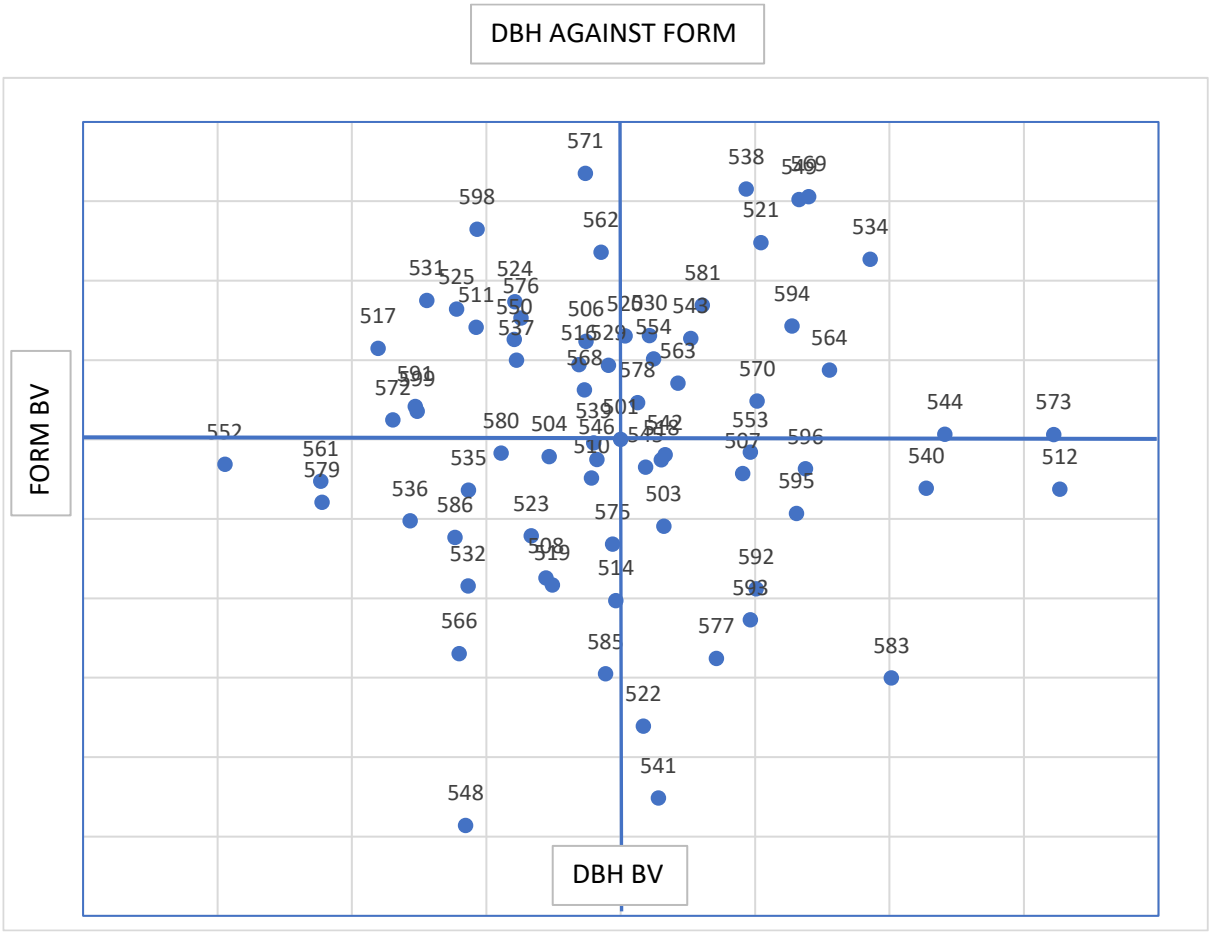

Figure 3: 3.5 year measurement of Paparoa Trial. Relationship between family breeding values for DBH and Form. Upper right quartile identifies the best families for these traits.

The sets of families planted in the 2011 and 2016 trials are unique and there are no linkages.

The Cuddons trial has been thinned and the poorest trees have been removed. The differences between families are not as pronounced. The average DBH across families ranged from 88.7mm to 113.3mm (Table 1). While the trees are five years older there has been slower growth than at the Paparoa site as the Cuddon site has very low rainfall.

Up to 20 trees with a diameter (DBH) above 50 mm were randomly selected from each family in the Cuddons trial. A bark to bark 14 mm diameter core through the pith was extracted at ~0.5 m stem height using a purpose-built corer in October 2020. The heartwood diameter in the stem was assessed by measuring the heartwood length in the core samples. Preliminary analysis of the data suggested heartwood quantity is under genetic control in this trial and not strongly correlated to tree diameter (Table 1.) indicating the need to consider heartwood quantity as an independent trait to DBH (Altaner and Ghildiyal, 2020). The evaluation of heartwood development is required in the 2016 trials when the trees have reached a suitable diameter and heartwood is evident.

Table 1: Results of 8.5 year measurement of families planted in Cuddons trial.

FAMILY	Provenance	Average DBH (mm)	Heartwood Ranking 1= Best
518	Dalmorton	105.4	1
516	Dalmorton	107.9	2
514	Clouds Creek	103.8	3
505	Mt Skanzi	103.2	4
519	Mt Skanzi	106.3	5
517	Dalmorton	97.8	6
507	Mt Skanzi	112.3	7
534	#N/A	103.3	8
512	Clouds Creek	88.7	9
504	Mt Skanzi	99.6	10
515	Dalmorton	102.4	11
520	Ben McNeil	109.2	12
513	Clouds Creek	98.7	13
509	Meryla SF	90.2	14
511	Clouds Creek	97.1	15
510	Clouds Creek	99.9	16
502	Dalmorton	110.9	17
501	Mt Skanzi	110.4	18
503	Mt Skanzi	108.1	19
506	Mt Skanzi	112.4	20
531	#N/A	113.3	21
508	Meryla SF	99.2	22
998	E.quad Control	113.0	6
996	E.bosis Control	126.0	2

CLONAL PROPAGATION

Following the harvesting operation of the trees planted at Murray's Nursery in the UC growth strain study coppice shoots were collected from the stumps for clonal propagation. 21 families were selected with below average growth-strain and above average growth. (Altaner, 2019). This equates to a selection intensity of 1 in 4 and is low compared to other breeding programs. However, it retains a broader genetic base for future selection to include health, heartwood content and propagation traits. In the future these selections can form the basis for industrial scale vegetative propagation from cuttings.

17 families were successfully captured from the collection of coppice material at Murray's Nursery. These clones have been managed by Proseed in the propagation facility at Amberley.

The list of families was reviewed in September 2020 using the results of the 3.5-year-old growth and form assessment of the Paparoa trial. Unfortunately not all the best families had been captured from coppice growth of the trees felled in the Woodville trial. The resulting group of 10 families (Table 2) are being propagated with the objective to produce 5,000 rooted cuttings for planting in 2021.

Table 2: Summary of breeding values (BV) for families of E. quadrangulata selected for cuttings propagation. Growth and form are results from Paparoa; Growth stress is from Woodville. DBH, STR (stem straightness), FORM at 3.5 years, HGT (total tree height) at 2.5 years, GS (Growth Stress) at 18 months.

FAMILY	Provenance	DBH_BV	HGT-BV	STR-BV	FORM-BV	GS-BV	No. Clones	Select Growth Stress	Select Growth Form
507	Dalmorton	4.532	0.542	0.137	-0.086	-51.697	5	Yes	
518	Giro SF	1.503	7.213	0.318	-0.051	-3.327	6	Yes	Yes
519	Giro SF	-2.545	0.804	-0.264	-0.367	-125.572	10	Yes	
520	Giro SF	0.162	0.288	0.112	0.261	7.015	8		Yes
521	Giro SF	5.211	2.813	-0.169	0.496	11.324	3		Yes
554	Sheas Nob SF	1.219	-0.873	0.035	0.203	-87.423	6	Yes	Yes
561	Chealundi SF	-11.158	-3.866	0.796	-0.105	-115.701	3	Yes	
577	Chealundi SF	3.555	-1.169	-0.144	-0.552	-32.584	2	Yes	
591	Giro SF	-7.647	-2.077	0.549	0.083	-121.634	3	Yes	
595	Giro SF	6.535	2.316	-0.621	-0.186	-131.379	1	Yes	

DISCUSSION

The target product for *E. quadrangulata* is ground durable timber or veneer and this will influence the importance of the selection traits. The top families for growth and form are not the same group that produce good heartwood volume. In 2016, Proseed grafted the best ortet of each family represented in the Cuddons trial. Up to 4 individuals were grafted of the best families based on 3.5 year old growth and form measurements. The clonal seed orchard located at Amberley can be rogued by Proseed to remove the very poor families for both growth and heartwood development. The further selection of families for the advancement of the breeding and deployment populations will be undertaken once assessments have been completed of the 2011 *E. quadrangulata* trial located in Hawkes Bay (DF0470_01Qua11) and 2016 *E. quadrangulata* trial located in Marlborough (DF0131_A_01Qua16).

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